

**Figure 4B**

10            20            30            40            50            60  
 .....|.....|.....|.....|.....  
**MGQCRSANAEDAQEFS**DVERAIETLIK**NFH**KYSVAGK**KETLTPA**ELRDLVTQQPLPHLMPS  
**MGQCRSANAEDAQEFS**DVERAIETLIK**NFH**OYSVGCK**KETLTPTSE**LRLDLVTQQPLPHLMPS  
**MGQCRSANAEDAQEFS**DVERAIETLIK**NFI**TYSV...G**KETLTPTSE**LRLDLVTQQPLPHLMPS

70 80 90 100  
 .....|.....|.....|.....|.....  
 NCGLEEKIANLGN CNDSDKLEFG SFWELIGEAAKSVKMERPV (SEQ ID NO:3)  
 NCGLEEKIANLGN CNDSDKLEFG SFWELIGEAAKSVKMERPV (SEQ ID NO:39)  
 NCGLEEKIANLGN CNDSDKLEFG SFWELIGEAAKSVKMERPV (SEQ ID NO:40)

[illegible]

70 80 90 100  
 NCGLEEKIANLGSCNDSKLEFRSFWELIGEAAKSVKLERPVRGH (SEQ ID NO:6)  
 NCGLEEKIANLGSCNDSKLEFRSFWELIGEAAKSVKLERPVRGH (SEQ ID NO:39)  
 NCGLEEKIANLGSCNDSKLEFRSFWELIGEAAKSVKLERPVRGH (SEQ ID NO:40)

[illegible]

Table 6

gi|4139958|pdb|1MHO

PROTEIN MRP-126

CALGRANULIN B

CALGRANULIN B

Consensus

10 20 30 40

SRLEHIDIKNFHQYSV-EGGNEILTPSSIRDLVTCOLPHLM (SEQ ID NO:6)

SRVAVVALIDVFHQYSGREGDKHRLKSELNELINNELSHFL (SEQ ID NO:41)

SRADIVLIDVFHQYSRREGQDILRLKELNLLEKOLANYL (SEQ ID NO:42)

ESSLEITINIVFHQYSVRLSHYDTLICKEFQLVOKELPNFL (SEQ ID NO:44)

ERSIITITIDVFHQYSRKEGHPOTLSRKEFRQMVFAQLATFM (SEQ ID NO:46)

SRLEHIDIKNFHQYS (SEQ ID NO:47)



Figure 7

*****Contig 1*****									
	.	:	.	:	.	:	.	:	.
65677221+	GAATTCAGAGGAGTTCTCAGTGGCCCCCGGACAGGCCCTCTCCAGCTTCACACTCTTGGC								
AA315020-	TGCCCCCGGACAGTCCCTCNAGCTTCACACTCTTGGC								
<b>consensus</b>	GAATTCAGAGGAGTTCTCAGTGGCCCCCGGACAGGCCCTCTCCAGCTTCACACTCTTGGC								
	.	:	.	:	.	:	.	:	.
65677221+	CGCTTCTCCAAATCAGCTCCCAGAAACTCCTGAACTCCAGTTTAGAGTCATTGCAGCTGCC								
AA315020-	CGCTTCTCCAAATCAGCTCCCAGAAACTCCTGAACTCCAGTTTAGAGTCATTGCAGCTGCC								
<b>consensus</b>	CGCTTCTCCAAATCAGCTCCCAGAAACTCCTGAACTCCAGTTTAGAGTCATTGCAGCTGCC								
	.	:	.	:	.	:	.	:	.
65677221+	CAGGTTGGCAATTTTCTCTTCCAGGCCACAGTTGCTCGGCATGAGATGGGGCAGCTGCTG								
AA315020-	CAGGTTGGCAATTTTCTCTTCCAGGCCANAGTTGCTCGGCATGAGATGGGGCAGCTGCTG								
<b>consensus</b>	CAGGTTGGCAATTTTCTCTTCCAGGCCACAGTTGCTCGGCATGAGATGGGGCAGCTGCTG								
	.	:	.	:	.	:	.	:	.
65677221+	GGTGACCAAGGTCCCGTAGCTCAGAAGGGGTACGGCTCTCCTTCCCACCCCTCCACGGAGTA								
AA315020-	GGTGACCAAGGTCCCGTAGCTCAGAAGGGGTACGGCTCTCCTTCCCACCCCTCCACGGAGTA								
<b>consensus</b>	GGTGACCAAGGTCCCGTAGCTCAGAAGGGGTACGGCTCTCCTTCCCACCCCTCCACGGAGTA								
	.	:	.	:	.	:	.	:	.
65677221+	CTGGTGAAAGTTCTTTGATGAGGGTCTCAATGGCCCTCTCCACATCACTGAATTC (SEQ ID NO: 37)								
AA315020-	CTGGTGAAAGTTCTTTGATGAGGGTCTCAATGGCCCTCTCCACATCACTGAATTCCTGAGC								
<b>consensus</b>	CTGGTGAAAGTTCTTTGATGAGGGTCTCAATGGCCCTCTCCACATCACTGAATTCCTGAGC								
	.	:	.	:	.	:	.	:	.
AA315020-	ATCCTCTGCGTTGGCTGACCGACACTGTCCCATGGTGCTCACTGTGTCTGGTCCCTTGGT								
<b>consensus</b>	ATCCTCTGCGTTGGCTGACCGACACTGTCCCATGGTGCTCACTGTGTCTGGTCCCTTGGT								
	.	:	.	:	.	:	.	:	.
AA315020-	GAGAGTTCTGTGTCTCTAT (SEQ ID NO: 49)								
<b>consensus</b>	GAGAGTTCTGTGTCTCTAT (SEQ ID NO: 5)								